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199 30 476.9	1 July 1999 (01.07.1999)	DE
60/142,101	2 July 1999 (02.07.1999)	US
199 31 415.2	8 July 1999 (08.07.1999)	DE
199 31 418.7	8 July 1999 (08.07.1999)	DE
199 31 419.5	8 July 1999 (08.07.1999)	DE
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199 33 006.9	14 July 1999 (14.07.1999)	DE
60/148,613	12 August 1999 (12.08.1999)	US
199 40 764.9	27 August 1999 (27.08.1999)	DE
199 40 765.7	27 August 1999 (27.08.1999)	DE
199 40 766.5	27 August 1999 (27.08.1999)	DE
199 40 832.7	27 August 1999 (27.08.1999)	DE
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199 41 394.0	31 August 1999 (31.08.1999)	DE
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199 41 380.0	31 August 1999 (31.08.1999)	DE
199 42 077.7	3 September 1999 (03.09.1999)	DE
199 42 129.3	3 September 1999 (03.09.1999)	DE
199 42 076.9	3 September 1999 (03.09.1999)	DE
199 42 079.3	3 September 1999 (03.09.1999)	DE
199 42 086.6	3 September 1999 (03.09.1999)	DE
199 42 087.4	3 September 1999 (03.09.1999)	DE
199 42 088.2	3 September 1999 (03.09.1999)	DE
199 42 095.5	3 September 1999 (03.09.1999)	DE
199 42 124.2	3 September 1999 (03.09.1999)	DE
60/187,970	9 March 2000 (09.03.2000)	US

(71) Applicant: BASF AKTIENGESELLSCHAFT [DE/DE]; D-67056 Ludwigshafen (DE).

(72) Inventors: [redacted] Markus; Wenjenstr. 21, D-67251 Freinsheim (DE). KRÖGER, Burkhard; Im Waldhof 1, D-67117 Limburgerhof (DE). SCHRÖDER, Hartwig; Goethestr. 5, D-69226 Nussloch (DE). ZELDER, Oskar; Rossmarktstr. 27, D-67346 Speyer (DE). HABERHAUER, Gregor; Moselstr. 42, D-67117 Limburgerhof (DE).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

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[Continued on next page]

(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.

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LOCUS AX063913 1170 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 195 from Patent WO0100843.
ACCESSION AX063913
VERSION AX063913.1 GI:12541625
KEYWORDS .
SOURCE Corynebacterium glutamicum.
ORGANISM Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
REFERENCE 1 (bases 1 to 1170)
AUTHORS Pompejus,M., Kroeger,B., Schroeder,H., Zelder,O. and Haberhauer,G.
TITLE corynebacterium glutamicum genes encoding metabolic pathway proteins
JOURNAL Patent: WO 0100843-A 195 04-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)

Query Match 99.9%; Score 1144.4; DB 6; Length 1170;
Best Local Similarity 99.9%; Pred. No. 2.4e-311;
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61 GTGCAAGCGGGACGGCCAGCCAGAACTCCTGGTGCGCCGATGAACCCACCTATCACGTTG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 GTGCAAGCGGGACGGCCAGCCAGAACTCCTGGTGCGCCGATGAACCCACCTATCACGTTG 121

Qy     121 TCCAGCACTTATGTTCATGATTCAGAAAAAGCTTATGGGCGCGATGGCAATGATGGATGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 TCCAGCACTTATGTTCATGATTCAGAAAAAGCTTATGGGCGCGATGGCAATGATGGATGG 181

Qy     181 GGTGCATTTGAGGCTGCCATGGGAACTCTAGATGGTGGGTTCGCGGTATCTTATTCTTCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 GGTGCATTTGAGGCTGCCATGGGAACTCTAGATGGTGGGTTCGCGGTATCTTATTCTTCA 241

Qy     241 GGTTTGGCAGCGGCAACGTCGATTGCTGATTTGGTTCCTACTGGTGGCACAGTTGTTTTA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 GGTTTGGCAGCGGCAACGTCGATTGCTGATTTGGTTCCTACTGGTGGCACAGTTGTTTTA 301

Qy     301 CCTAAAGCTGCCTATTATGGCGTGACCAATATTTTCGCCAGGATGGAAGCCCGCGGAAGG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 CCTAAAGCTGCCTATTATGGCGTGACCAATATTTTCGCCAGGATGGAAGCCCGCGGAAGG 361

Qy     361 CTGAAGGTTCGAACTGTTGATGCAGACAATACCGAAGAAGTGATTGCTGCTGCTCAAGGT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 CTGAAGGTTCGAACTGTTGATGCAGACAATACCGAAGAAGTGATTGCTGCTGCTCAAGGT 421

Qy     421 GCAGATGTGGTGTGGGTGGAATCGATCGCTAATCCGACGATGGTGGTAGCTGATATCCCT 480
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Db     422 GCAGATGTGGTGTGGGTGGAATCGATCGCTAATCCGACGATGGTGGTAGCTGATATCCCT 481

Qy     481 GCAATAGTCGACGGTGTGCGTGGGCTTGGAGTTTTGACTGTCGTTGACGCGACTTTCGCA 540
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Db     482 GCAATAGTCGACGGTGTGCGTGGGCTTGGAGTTTTGACTGTCGTTGACGCGACTTTCGCA 541
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Qy        541 ACGCCACTTCGTCAACGTCCATTGGAACTTGGTGCTGATATTGTGCTTTACTCGGCAACC 600
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Db        542 ACGCCACTTCGTCAACGTCCATTGGAACTTGGTGCTGATATTGTGCTTTACTCGGCAACC 601

Qy        601 AAACTTATCGGTGGACACTCTGATCTTCTTCTTGGAGTCGCAGTGTGCAAGTCTGAGCAC 660
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Db        602 AAACTTATCGGTGGACACTCTGATCTTCTTCTTGGAGTCGCAGTGTGCAAGTCTGAGCAC 661

Qy        661 CATGCGCAGTTTCTTGCCACTCACCGTCATGATCATGGTTCAGTGCCGGGAGGTCTTGAA 720
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Db        662 CATGCGCAGTTTCTTGCCACTCACCGTCATGATCATGGTTCAGTGCCGGGAGGTCTTGAA 721

Qy        721 GCGTTTCTTGCTCTCCGTGGATTGTATTCCTTGGCGGTGCGTCTTGATCGAGCAGAATCC 780
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Db        722 GCGTTTCTTGCTCTCCGTGGATTGTATTCCTTGGCGGTGCGTCTTGATCGAGCAGAATCC 781

Qy        781 AACGCAGCAGAACTTTCGCGGCGACTTAACGCGCATCCTTCGGTTACCCGCGTCAATTAT 840
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Db        782 AACGCAGCAGAACTTTCGCGGCGACTTAACGCGCATCCTTCGGTTACCCGCGTCAATTAT 841

Qy        841 CCAGGACTTCCTGATGATCCCCAACATGAAAAAGCCGTGCGAGTCCTACCCTCTGGATGT 900
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Qy        901 GGAAACATGTTGTCATTTGAGCTTGATGCAACACCTGAACGAACTGATGAGATTCTCGAA 960
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Db        902 GGAAACATGTTGTCATTTGAGCTTGATGCAACACCTGAACGAACTGATGAGATTCTCGAA 961

Qy        961 AGCCTGTCACTTTTAACCCACGCGACCAGTTGGGGAGGTGTGGAAACAGCCATTGAACGT 1020
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Db        962 AGCCTGTCACTTTTAACCCACGCGACCAGTTGGGGAGGTGTGGAAACAGCCATTGAACGT 1021

Qy       1021 CGCACCAGGCGGGATGCTGAAGTGGTGGCAGGAGTACCGATGACTCTTTGCCGCGTTTCC 1080
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1022 CGCACCAGGCGGGATGCTGAAGTGGTGGCAGAAGTACCGATGACTCTTTGCCGCGTTTCC 1081

Qy       1081 GTAGGAATTGAAGACGTTGAAGATCTATGGGAAGACCTCAACGCCTCAATCGACAAAGTT 1140
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Db       1082 GTAGGAATTGAAGACGTTGAAGATCTATGGGAAGACCTCAACGCCTCAATCGACAAAGTT 1141

Qy       1141 CTGGGT 1146
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Db       1142 CTGGGT 1147
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LOCUS AX063913 1170 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 195 from Patent WO0100843.
ACCESSION AX063913
VERSION AX063913.1 GI:12541625
KEYWORDS .
SOURCE Corynebacterium glutamicum.
ORGANISM Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
REFERENCE 1 (bases 1 to 1170)
AUTHORS Pompejus,M., Kroeger,B., Schroeder,H., Zelder,O. and Haberhauer,G.
TITLE corynebacterium glutamicum genes encoding metabolic pathway proteins
JOURNAL Patent: WO 0100843-A 195 04-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)

Alignment Scores:

Pred. No.:	4.9e-119	Length:	1170
Score:	1960.00	Matches:	381
Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	1
Query Match:	99.59%	Indels:	0
DB:	6	Gaps:	0

US-09-919-831-3 (1-382) x AX063913 (1-1170)

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Db          2 ATGAATTTTTACCCACCATCTGTACCTATTAACCCTGCGTGGCGTCCACCCACAGTAACT 61

Qy         21 ValGlnAlaGlyArgProAlaArgThrProGlyAlaProMetAsnProProIleThrLeu 40
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Db         62 GTGCAAGCGGGACGGCCAGCCAGAACTCCTGGTGCGCCGATGAACCCACCTATCACGTTG 121

Qy         41 SerSerThrTyrValHisAspSerGluLysAlaTyrGlyArgAspGlyAsnAspGlyTrp 60
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Db        122 TCCAGCACTTATGTTCATGATTCAGAAAAAGCTTATGGGCGCGATGGCAATGATGGATGG 181

Qy         61 GlyAlaPheGluAlaAlaMetGlyThrLeuAspGlyGlyPheAlaValSerTyrSerSer 80
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Qy         81 GlyLeuAlaAlaAlaThrSerIleAlaAspLeuValProThrGlyGlyThrValValLeu 100
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Db        242 GGTTTGGCAGCGGCAACGTCGATTGCTGATTTGGTTCCTACTGGTGGCACAGTTGTTTTA 301

Qy        101 ProLysAlaAlaTyrTyrGlyValThrAsnIlePheAlaArgMetGluAlaArgGlyArg 120
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Db        302 CCTAAAGCTGCCTATTATGGCGTGACCAATATTTTCGCCAGGATGGAAGCCCGCGGAAGG 361

Qy        121 LeuLysValArgThrValAspAlaAspAsnThrGluGluValIleAlaAlaAlaGlnGly 140
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Db        362 CTGAAGGTTCGAACTGTTGATGCAGACAATACCGAAGAAGTGATTGCTGCTGCTCAAGGT 421

Qy        141 AlaAspValValTrpValGluSerIleAlaAsnProThrMetValValAlaAspIlePro 160
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Db        482 GCAATAGTCGACGGTGTGCGTGGGCTTGGAGTTTTGACTGTCGTTGACGCGACTTTCGCA 541

Qy        181 ThrProLeuArgGlnArgProLeuGluLeuGlyAlaAspIleValLeuTyrSerAlaThr 200
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Qy        201 LysLeuIleGlyGlyHisSerAspLeuLeuLeuGlyValAlaValCysLysSerGluHis 220
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Qy        261 AsnAlaAlaGluLeuSerArgArgLeuAsnAlaHisProSerValThrArgValAsnTyr 280
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Db        782 AACGCAGCAGAACTTTCGCGGCGACTTAACGCGCATCCTTCGGTTACCCGCGTCAATTAT 841

Qy        281 ProGlyLeuProAspAspProGlnHisGluLysAlaValArgValLeuProSerGlyCys 300
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Db        842 CCAGGACTTCCTGATGATCCCCAACATGAAAAAGCCGTGCGAGTCCTACCCTCTGGATGT 901

Qy        301 GlyAsnMetLeuSerPheGluLeuAspAlaThrProGluArgThrAspGluIleLeuGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GGAAACATGTTGTCATTTGAGCTTGATGCAACACCTGAACGAACTGATGAGATTCTCGAA 961

Qy        321 SerLeuSerLeuLeuThrHisAlaThrSerTrpGlyGlyValGluThrAlaIleGluArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 AGCCTGTCACTTTTAACCCACGCGACCAGTTGGGGAGGTGTGGAAACAGCCATTGAACGT 1021

Qy        341 ArgThrArgArgAspAlaGluValValAlaGlyValProMetThrLeuCysArgValSer 360
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db       1022 CGCACCAGGCGGGATGCTGAAGTGGTGGCAGAAGTACCGATGACTCTTTGCCGCGTTTCC 1081

Qy        361 ValGlyIleGluAspValGluAspLeuTrpGluAspLeuAsnAlaSerIleAspLysVal 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        381 LeuGly 382
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